



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/018,929B  
Source: 1FW16  
Date Processed by STIC: 8/6/04

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~  
~~VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND~~  
~~TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:~~

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202



IFW16

## RAW SEQUENCE LISTING

DATE: 08/06/2004

PATENT APPLICATION: US/10/018,929B

TIME: 11:19:55

Input Set : A:\Second Corrected Sequence Listing 5-2002.txt

Output Set: N:\CRF4\08062004\J018929B.raw

4 <110> APPLICANT: Novartis AG  
 5 Novartis Research Foundation  
 7 <120> TITLE OF INVENTION: Gene involved in epigenetic gene silencing  
 9 <130> FILE REFERENCE: S-31005A  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/018,929B  
 C--> 12 <141> CURRENT FILING DATE: 2001-12-21  
 14 <150> PRIOR APPLICATION NUMBER: GB 9914623.5  
 15 <151> PRIOR FILING DATE: 1999-06-23  
 E--> 17 <160> NUMBER OF SEQ ID NOS: 33 (see below)  
 19 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply  
 Corrected Diskette Needed

## ERRORED SEQUENCES

1641 <210> SEQ ID NO: 34 *last sequence in submitted file*  
 1642 <211> LENGTH: 8  
 1643 <212> TYPE: PRT  
 1644 <213> ORGANISM: Artificial Sequence  
 1646 <220> FEATURE:  
 1647 <222> LOCATION: 1..8  
 1648 <223> OTHER INFORMATION: ATP/GTP-binding motif A consensus sequence  
 1650 <220> FEATURE:  
 1651 <222> LOCATION: 1  
 1652 <223> OTHER INFORMATION: Xaa= Ala or Gly  
 1654 <220> FEATURE:  
 1655 <222> LOCATION: 2..5 *5 ← (give correct locations)*  
 1656 <223> OTHER INFORMATION: Xaa= any amino acid  
 1658 <220> FEATURE:  
 1659 <222> LOCATION: 8  
 1660 <223> OTHER INFORMATION: Xaa= Ser or Thr  
 1662 <400> SEQUENCE: 34  
 V--> 1663 Xaa Xaa Xaa Xaa Xaa Gly Lys Xaa  
 E--> 1664 1 5

~~10~~ ~~15~~  
*delete - do not include these  
 amino acid numbers if no  
 amino acid is above them.*

VARIABLE LOCATION SUMMARY  
PATENT APPLICATION: US/10/018,929B

DATE: 08/06/2004  
TIME: 11:19:56

Input Set : A:\Second Corrected Sequence Listing 5-2002.txt  
Output Set: N:\CRF4\08062004\J018929B.raw

YI  
Presence of n's or Xaa's (NEW RULES):

Presence of n's and/or Xaa's have been detected in the Sequence Listing.

Presence of <220> to <223> is MANDATORY if n's or Xaa's are present.

<220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

q#:7; N Pos. 1  
q#:8; N Pos. 1,11  
q#:9; N Pos. 5,10,13  
q#:10; N Pos. 6,13  
q#:11; N Pos. 11,13  
q#:12; N Pos. 4,8,13  
q#:13; N Pos. 6,8,13  
q#:26; N Pos. 10,11  
q#:34; Xaa Pos. 4,2,3,4,5,8

## VERIFICATION SUMMARY

DATE: 08/06/2004

PATENT APPLICATION: US/10/018,929B

TIME: 11:19:56

Input Set : A:\Second Corrected Sequence Listing 5-2002.txt

Output Set: N:\CRF4\08062004\J018929B.raw

M:270 C: Current Application Number differs, Replaced Application Number  
M:271 C: Current Filing Date differs, Replaced Current Filing Date  
43 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7  
43 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7  
43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0  
57 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:8  
57 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8  
57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0  
71 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:9  
71 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9  
71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
85 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:10  
85 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:10  
85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0  
99 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:11  
99 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:11  
99 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
13 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:12  
13 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:12  
13 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
27 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13  
27 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:13  
27 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
96 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:26  
96 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:26  
96 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0  
63 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:34  
63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0  
64 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:34  
M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (33) Counted (34)